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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/016,668

DATE: 05/06/2002

TIME: 14:21:53

Input Set : A:\Sequence Listing (ASCII copy).txt

Output Set: N:\CRF3\05062002\J016668.raw

3 <110> APPLICANT: Wang, Zhen-Gang
4 Voigt, Christopher A.
5 Mayo, Stephen L.
6 Arnold, Frances H.
8 <120> TITLE OF INVENTION: GENE RECOMBINATION AND HYBRID PROTEIN DEVELOPMENT
10 <130> FILE REFERENCE: 9373/1H812-US3
12 <140> CURRENT APPLICATION NUMBER: US 10/016,668
C--> 13 <141> CURRENT FILING DATE: 2002-04-22
15 <150> PRIOR APPLICATION NUMBER: US 09/863,765
16 <151> PRIOR FILING DATE: 2001-05-23
18 <150> PRIOR APPLICATION NUMBER: US 60/207,048
19 <151> PRIOR FILING DATE: 2000-05-23
21 <150> PRIOR APPLICATION NUMBER: US 60/235,960
22 <151> PRIOR FILING DATE: 2000-09-27
24 <150> PRIOR APPLICATION NUMBER: US 60/283,567
25 <151> PRIOR FILING DATE: 2001-04-13
27 <160> NUMBER OF SEQ ID NOS: 6
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 361
33 <212> TYPE: PRT
34 <213> ORGANISM: Enterobacter cloacae
36 <300> PUBLICATION INFORMATION:
37 <308> DATABASE ACCESSION NO: SWIS-PROT / P05364
38 <309> DATABASE ENTRY DATE: 1988-11-09
39 <313> RELEVANT RESIDUES: (1)..(361)
41 <400> SEQUENCE: 1
43 Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile
44 1 5 10 15
47 Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met Ala Val Ala Val
48 20 25 30
51 Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile
52 35 40 45
55 Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser
56 50 55 60
59 Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
60 65 70 75 80
63 Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu
64 85 90 95
67 Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr
68 100 105 110
71 Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn
72 115 120 125

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75 Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro
76      130      135      140
79 Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala
80 145      150      155      160
83 Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr
84      165      170      175
87 Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro
88      180      185      190
91 Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala
92      195      200      205
95 Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys
96      210      215      220
99 Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala Asn Met Ala Pro
100 225      230      235      240
103 Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln
104      245      250      255
107 Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu
108      260      265      270
111 Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val Glu Gly Ser Asp
112      275      280      285
115 Ser Lys Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro
116      290      295      300
119 Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly
120 305      310      315      320
123 Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile
124      325      330      335
127 Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala
128      340      345      350
131 Ala Tyr His Ile Leu Glu Ala Leu Gln
132      355      360
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 361
137 <212> TYPE: PRT
138 <213> ORGANISM: Citrobacter freundii
140 <300> PUBLICATION INFORMATION:
141 <308> DATABASE ACCESSION NO: SWIS-PROT / P05193
142 <309> DATABASE ENTRY DATE: 1987-08-05
143 <313> RELEVANT RESIDUES: (1)..(361)
145 <400> SEQUENCE: 2
147 Ala Ala Lys Thr Glu Gln Gln Ile Ala Asp Ile Val Asn Arg Thr Ile
148 1      5      10      15
151 Thr Pro Leu Met Gln Glu Gln Ala Ile Pro Gly Met Ala Val Ala Ile
152      20      25      30
155 Ile Tyr Glu Gly Lys Pro Tyr Tyr Phe Thr Trp Gly Lys Ala Asp Ile
156      35      40      45
159 Ala Asn Asn His Pro Val Thr Gln Gln Thr Leu Phe Glu Leu Gly Ser
160      50      55      60
163 Val Ser Lys Thr Phe Asn Gly Val Leu Gly Gly Asp Arg Ile Ala Arg
164 65      70      75      80

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167 Gly Glu Ile Lys Leu Ser Asp Pro Val Thr Lys Tyr Trp Pro Glu Leu
168      85      90      95
171 Thr Gly Lys Gln Trp Arg Gly Ile Ser Leu Leu His Leu Ala Thr Tyr
172      100     105     110
175 Thr Ala Gly Gly Leu Pro Leu Gln Ile Pro Gly Asp Val Thr Asp Lys
176      115     120     125
179 Ala Glu Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Thr Pro
180      130     135     140
183 Gly Ala Lys Arg Leu Tyr Ala Asn Ser Ser Ile Gly Leu Phe Gly Ala
184 145      150      155      160
187 Leu Ala Val Lys Ser Ser Gly Met Ser Tyr Glu Glu Ala Met Thr Arg
188      165     170     175
191 Arg Val Leu Gln Pro Leu Lys Leu Ala His Thr Trp Ile Thr Val Pro
192      180     185     190
195 Gln Ser Glu Gln Lys Asn Tyr Ala Trp Gly Tyr Leu Glu Gly Lys Pro
196      195     200     205
199 Val His Val Ser Pro Gly Gln Leu Asp Ala Glu Ala Tyr Gly Val Lys
200      210     215     220
203 Ser Ser Val Ile Asp Met Ala Arg Trp Val Gln Ala Asn Met Asp Ala
204 225      230     235     240
207 Ser His Val Gln Glu Lys Thr Leu Gln Gln Gly Ile Glu Leu Ala Gln
208      245     250     255
211 Ser Arg Tyr Trp Arg Ile Gly Asp Met Tyr Gln Gly Leu Gly Trp Glu
212      260     265     270
215 Met Leu Asn Trp Pro Leu Lys Ala Asp Ser Ile Ile Asn Gly Ser Asp
216      275     280     285
219 Ser Lys Val Ala Leu Ala Ala Leu Pro Ala Val Glu Val Asn Pro Pro
220      290     295     300
223 Ala Pro Ala Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly
224 305      310     315     320
227 Gly Phe Gly Ser Tyr Val Ala Phe Val Pro Glu Lys Asn Leu Gly Ile
228      325     330     335
231 Val Met Leu Ala Asn Lys Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala
232      340     345     350
235 Ala Trp Arg Ile Leu Glu Lys Leu Gln
236      355     360
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 361
241 <212> TYPE: PRT
242 <213> ORGANISM: Yersinia enterocolitica
244 <300> PUBLICATION INFORMATION:
245 <308> DATABASE ACCESSION NO: SWIS-PROT / P45460
246 <309> DATABASE ENTRY DATE: 1995-11-01
247 <313> RELEVANT RESIDUES: (1)..(361)
249 <400> SEQUENCE: 3
251 Thr Lys Leu Thr Glu Leu Gln Val Ala Thr Ile Val Asn Asn Thr Leu
252 1      5      10      15
255 Thr Pro Leu Leu Glu Lys Gln Gly Ile Pro Gly Met Ala Val Ala Val
256      20      25      30

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259 Phe Tyr Asp Gly Lys Pro Gln Phe Phe Asn Tyr Gly Met Ala Asp Ile
260           35           40           45
263 Lys Ala Gly Arg Pro Val Thr Glu Asn Thr Leu Phe Glu Leu Gly Ser
264           50           55           60
267 Val Ser Lys Thr Phe Thr Gly Val Ala Gly Glu Tyr Ala Met Gln Thr
268 65           70           75           80
271 Gly Ile Met Asn Leu Asn Asp Pro Val Thr Glu Tyr Ala Pro Glu Leu
272           85           90           95
275 Thr Gly Ser Gln Trp Lys Asp Val Lys Met Leu His Leu Ala Thr Tyr
276           100          105          110
279 Thr Ala Gly Gly Leu Pro Leu Gln Leu Pro Asp Ser Val Thr Asp Gln
280           115          120          125
283 Lys Ser Leu Trp Gln Tyr Tyr Gln Gln Trp Gln Pro Gln Trp Ala Pro
284           130          135          140
287 Gly Val Met Arg Asn Tyr Ser Asn Ala Ser Ile Gly Leu Phe Gly Ala
288 145          150          155          160
291 Leu Ala Val Lys Arg Ser Gln Leu Thr Phe Glu Asn Tyr Met Lys Glu
292           165          170          175
295 Tyr Val Phe Gln Pro Leu Lys Leu Asp His Thr Phe Ile Thr Ile Pro
296           180          185          190
299 Glu Ser Met Gln Ser Asn Tyr Ala Trp Gly Tyr Lys Asp Gly Gln Pro
300           195          200          205
303 Val Arg Val Thr Leu Gly Met Leu Gly Glu Glu Ala Tyr Gly Val Lys
304           210          215          220
307 Ser Thr Ser Gln Asp Met Val Arg Phe Met Gln Ala Asn Met Asp Pro
308 225          230          235          240
311 Glu Ser Leu Gly Asn Asp Lys Leu Lys Glu Ala Ile Ile Ala Ser Gln
312           245          250          255
315 Ser Arg Tyr Phe Gln Ala Gly Asp Met Phe Gln Gly Leu Gly Trp Glu
316           260          265          270
319 Met Tyr Ser Trp Pro Ile Asn Pro Gln Gly Val Ile Ala Asp Ser Gly
320           275          280          285
323 Asn Asp Ile Ala Leu Lys Pro Arg Lys Val Glu Ala Leu Val Pro Ala
324           290          295          300
327 Gln Pro Ala Val Arg Ala Ser Trp Val His Lys Thr Gly Ala Thr Asn
328 305          310          315          320
331 Gly Phe Gly Ala Tyr Ile Val Phe Ile Pro Glu Glu Lys Val Gly Ile
332           325          330          335
335 Val Met Leu Ala Asn Lys Asn Tyr Pro Asn Pro Val Arg Val Gln Ala
336           340          345          350
339 Ala Tyr Asp Ile Leu Gln Ala Leu Arg
340           355          360
343 <210> SEQ ID NO: 4
344 <211> LENGTH: 359
345 <212> TYPE: PRT
346 <213> ORGANISM: Klebsiella pneumoniae
348 <300> PUBLICATION INFORMATION:
349 <308> DATABASE ACCESSION NO: SWISPROT / Q48437
350 <309> DATABASE ENTRY DATE: 1996-11-01

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351 <313> RELEVANT RESIDUES: (1)..(359)

353 <400> SEQUENCE: 4

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355 Tyr Ala Arg Gly Glu Ala Pro Leu Thr Ala Ala Val Asp Gly Ile Ile
356 1          5          10          15
359 Gln Pro Met Leu Lys Glu Tyr Arg Ile Pro Gly Met Ala Val Ala Val
360          20          25          30
363 Leu Lys Asp Gly Lys Ala His Tyr Phe Asn Tyr Gly Val Ala Asn Arg
364          35          40          45
367 Glu Ser Gly Gln Arg Val Ser Glu Gln Thr Leu Phe Glu Ile Gly Ser
368          50          55          60
371 Val Ser Lys Thr Leu Thr Ala Thr Leu Gly Ala Tyr Ala Ala Val Lys
372 65          70          75          80
375 Gly Gly Phe Glu Leu Asp Asp Lys Val Ser Gln His Ala Pro Trp Leu
376          85          90          95
379 Lys Gly Ser Ala Phe Asp Gly Val Thr Met Ala Glu Leu Ala Thr Tyr
380          100          105          110
383 Ser Ala Gly Gly Leu Pro Leu Gln Phe Pro Asp Glu Val Asp Ser Asn
384          115          120          125
387 Asp Lys Met Arg Thr Tyr Tyr Arg His Trp Ser Pro Val Tyr Pro Ala
388          130          135          140
391 Gly Thr His Arg Gln Tyr Ser Asn Pro Ser Ile Gly Leu Phe Gly His
392 145          150          155          160
395 Leu Ala Ala Asn Ser Leu Gly Gln Pro Phe Glu Gln Leu Met Ser Gln
396          165          170          175
399 Thr Leu Leu Pro Lys Leu Gly Leu His His Thr Tyr Ile Gln Val Pro
400          180          185          190
403 Glu Ser Ala Ile Ala Asn Tyr Ala Tyr Gly Tyr Lys Glu Asp Lys Pro
404          195          200          205
407 Val Arg Val Thr Pro Gly Val Leu Ala Ala Glu Ala Tyr Gly Ile Lys
408          210          215          220
411 Thr Gly Ser Ala Asp Leu Leu Lys Phe Thr Glu Ala Asn Met Gly Tyr
412 225          230          235          240
415 Gln Gly Asp Ala Ala Leu Lys Thr Arg Ile Ala Leu Thr His Thr Gly
416          245          250          255
419 Phe Tyr Ser Val Gly Asp Met Thr Gln Gly Leu Gly Trp Glu Ser Tyr
420          260          265          270
423 Ala Tyr Pro Leu Thr Glu Gln Ala Leu Leu Ala Gly Asn Ser Pro Ala
424          275          280          285
427 Val Ser Phe Gln Ala Asn Pro Val Thr Arg Phe Ala Val Pro Lys Ala
428          290          295          300
431 Met Gly Glu Gln Arg Leu Tyr Asn Lys Thr Gly Ser Thr Gly Gly Phe
432 305          310          315          320
435 Gly Ala Tyr Val Ala Phe Val Pro Ala Arg Gly Ile Ala Ile Val Met
436          325          330          335
439 Leu Ala Asn Arg Asn Tyr Pro Ile Glu Ala Arg Val Lys Ala Ala His
440          340          345          350
443 Ala Ile Leu Ser Gln Leu Ala
444          355
447 <210> SEQ ID NO: 5

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VERIFICATION SUMMARY

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